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receptor for Sonic hedgehog (SHH).  
 - SUBCELLULAR LOCATION: Integral membrane protein  
 - TISSUE SPECIFICITY: Expressed in epithelial cells of the developing hair, tooth and whisker.  
 - DEVELOPMENTAL STAGE: Detected in 8.5 to 17.5 dpc embryos.  
 - SIMILARITY: Belongs to the patched family.  
 - SIMILARITY: Contains 1 sterol-sensing (SSD) domain.

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EMBL; AB010833; BAA24691.1; -.  
 PIR; T13952; T13952.  
 MGD; MGI:1095405; Ptch2.  
 InterPro; IPR03392; Patched.  
 InterPro; IPR004766; Patchedm\_recept.  
 PFam; PF04260; Patched.  
 DR; TIGR918; TIGR918; 2a060602; 1.  
 PROSITE; PSS0156; SSD; 1.  
 KW; GLycoprotein; Receptor; Transmembrane.  
 DOMAIN; 1; Cytoplasmic (Potential).  
 FT; TRANSEM; 58; 78; Extracellular (Potential).  
 FT; TRANSEM; 79; 394; Potentail.  
 FT; TRANSEM; 395; 414; Cytoplasmic (Potential).  
 FT; TRANSEM; 415; 428; Potential.  
 FT; TRANSEM; 439; 449; Extracellular (Potential).  
 FT; TRANSEM; 450; 457; Extracellular (Potential).  
 FT; TRANSEM; 458; 478; Potentail.  
 FT; DOMAIN; 479; 501; Cytoplasmic (Potential).  
 FT; TRANSEM; 502; 522; Extracellular (Potential).  
 FT; DOMAIN; 523; 531; Potentail.  
 FT; TRANSEM; 532; 552; Extracellular (Potential).  
 FT; DOMAIN; 553; 686; Cytoplasmic (Potential).  
 FT; TRANSEM; 687; 707; Potentail.  
 FT; DOMAIN; 708; 963; Extracellular (Potential).  
 FT; TRANSEM; 964; 984; Potentail.  
 FT; DOMAIN; 985; 991; Cytoplasmic (Potential).  
 FT; TRANSEM; 992; 1012; Extracellular (Potential).  
 FT; DOMAIN; 1013; 1013; Potentail.  
 FT; TRANSEM; 1014; 1034; Extracellular (Potential).  
 FT; DOMAIN; 1035; 1064; Cytoplasmic (Potential).  
 FT; TRANSEM; 1065; 1085; Extracellular (Potential).  
 FT; DOMAIN; 1086; 1086; Potentail.  
 FT; TRANSEM; 1087; 1107; Cytoplasmic (Potential).  
 FT; DOMAIN; 1108; 1182; Extracellular (Potential).  
 FT; TRANSEM; 1109; 552; SSD.  
 FT; DOMAIN; 1014; 1034; N-linked (GlcNAc. . .) (Potential).  
 FT; CARBOHYD; 370; 370; N-linked (GlcNAc. . .) (Potential).  
 SQ; SEQUENCE; 1182; AA; 128585 MW; 715233912C52F2 CRC64;

Query Match 89.3%; Score: 599; DB 1; Length 1182;  
 Best Local Similarity 90.9%; Pred. No. 0; Indels 0; Gaps 0;  
 Matches 1074; Conservative 43; Mismatches 64;

QY; 1 MTRSPDPLLPSPSYTPARTAAPQILASLAKPLWIRAYFOGLLSFGGGIQRHCGKVLF 60  
 DB; 1 MVRPLSLGLBLLPSYTPARSSAPHAGSLQAPLNRAYFOGLLFSIGGRIQRHCGKVLF 60

QY; 61 LGLLAFLGALALGERMATEETNILEQLNWVEGRVSOPLHHTKKGLEBAMYTSOMLIONAR 120  
 DB; 61 LGLVAFGLALGLRVAVIETDLEQLNVEYGRSVQELHYTKEKGEBARYTSMQMLQTAH 120

QY; 121 QEGENILPTEALGLLHQALQALTAQVONSLYCKSMDLNK1CYKSYVPLENGMBMIEKL 180  
 DB; 121 QEGENVLTPEALGLLHQALQALTAQVONSLYCKSMDLNK1CYKSYVPLENGMBMIEKL 180

QY; 121 QEGENVLTPEALGLLHQALQALTAQVONSLYCKSMDLNK1CYKSYVPLENGMBMIEKL 180  
 DB; 121 QEGENVLTPEALGLLHQALQALTAQVONSLYCKSMDLNK1CYKSYVPLENGMBMIEKL 180

QY; 181 PPCVILTPDCFMEGAKLQGGSSAYLPPRDIQWTNDDPEQUBBZGPPASLBGFREILDK 240

RESUME 6  
 CACB8120  
 ID CACB8120  
 AC CACB8120  
 DT 02-MAR-2004 (TRIMBLrel. 27, Created)

421 SGSGVGLAGLVLVALAVASGLCAGLGTENAAATTQVLPFLALIGTYDGVFLLAHAFTF 480  
 421 SGSGVGLAGLVLVALAVASGLCAGLGTENAAATTQVLPFLALIGTYDGVFLLAHAFTF 480

421 FPCVILTPDCFMEGAKLQGGSSAYLPPRDIQWTNDDPEQUBBZGPPASLBGFREILDK 240  
 241 AOVQAYYGRPLHPPDHCPSAPTHSROAPNTAHELSGGCHGFSIKHCFMHQEELLG 300  
 241 AOVQAYYGRPLHPPDHCPSAPTHSROAPNTAHELSGGCHGFSIKHCFMHQEELLG 300  
 301 GMARDPOGBLLRABALOSTFLMSPROLYERFRGDYQTHDGINSEQEASTVLAQWRRFV 360  
 301 GTRDLOGLLRAENLOSTFLMSPROLYERFRGDYQTHDGINSEQEASTVLAQWRRFV 360  
 361 QLAQBALPENASQIHFASSTTDLHAFSEASARVYGGYLMLAACVTLRNDCAQ 420  
 361 QLAQBALPENASQIHFASSTTDLHAFSEASARVYGGYLMLAACVTLRNDCAQ 420  
 421 SOGSVGLAGLVLVALAVASGLCAGLGTENAAATTQVLPFLALIGTYDGVFLLAHAFTF 480  
 421 SGSGVGLAGLVLVALAVASGLCAGLGTENAAATTQVLPFLALIGTYDGVFLLAHAFTF 480

481 ALPOTPLPERMGECLQRTGTSVYLTSINNMRAFLMAMALVPIPAIRFLSIQALIVGGCTFV 540  
 481 APPDPLPERMGECLQRTGTSVYLTSINNMRAFLMAMALVPIPAIRFLSIQALIVGGCTFV 540  
 541 AVNLVFPAILSPDLRRHRCQRLDVLCCFSSSPCSAGVQITLPOBLGDTVPVGIAHLATV 600  
 541 AVNLVFPAILSPDLRRHRCQRLDVLCCFSSSPCSAQVQITLPOBLGDTVPVGIAHLATV 600  
 601 QAFTHCEASSQVTVLIPQAHLPVPPSDLGSELFSPGSTRDLQGELQTRQAKLVLFFSBL 660  
 601 QAFTHCEASSQVTVLIPQAHLPVPPSDLGSELFSPGSTRDLQGELQTRQAKLVLFFSBL 660  
 661 LPCARWNLAHFARYQFAPLILQSHAKAIVLVLFGALGSLYCATLVDGLALTDVPRG 720  
 661 LCAHWTLAHFARYQFAPLILQSHAKAIVLVLFGALGSLYCATLVDGLALTDVPRG 720  
 721 TKEHAFUSAQLYPSLIVBVLYTQGFDYAHQSRLDHFQHRSLLKAVLPPATQAPRT 780  
 721 TKEHAFUSAQLYPSLIVBVLYTQGFDYAHQSRLDHFQHRSLLKAVLPPATQAPRT 780  
 781 WLEYTRWNLQGQAFQDQDMSAGRITRHSYRNGSDGALAYKULIQTQGDAQQLPDLFSQLT 840  
 781 WLEYTRWNLQGQAFQDQDMSAGRITRHSYRNGSDGALAYKULIQTQGDAQQLPDLFSQLT 840  
 901 PAPPLEFQQPFPLLRGQIQTADFVEAIEGARAACAGDAGVHAYPPSSPFLEWQTLGL 960  
 901 AAQPLEFQQPFPLLRGQIQTADFVEAIEGARAACAGDAGVHAYPPSSPFLEWQTLGL 960  
 961 RRCPLLAVCILLLVCTFLVCAILLNWTAGLIVLWAMTVELGIMQFLGIKLSAIPVV 1020  
 961 RRCPLLAVCILLLVCTFLVCAILLNWTAGLIVLWAMTVELGIMQFLGIKLSAIPVV 1020  
 1021 ILVAVSGIGVVEPTVHAGLFTTQSSRNRAHALENTEAPYDGAISTLGLLMLAGSH 1080  
 1021 ILVAVSGIGVVEPTVHAGLFTTQSSRNRAHALENTEAPYDGAISTLGLLMLAGSN 1080

QY; 1081 FDPTRVFFRAAFTVLLTGLLGLLQKQIATVYKSETEILSPPAQQGG 1140  
 DB; 1081 FDPTRVFFWVLTGLLGLLQKQIATVYKSETEILSPPAQQGG 1140  
 QY; 1141 LRGASSSSLQSPARNTTSMTVAIHPPEPGAYTHAPDEP 1181  
 DB; 1141 LRDRPPTLQSPARNTTSMTVAIHPPEPGAYTHAPDEP 1181

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